

GenCore version 4.1  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 08:57:26, Search time: 11.1 seconds  
(without all repeats)  
1999-722 million (0.1) updates/sec

Title: US-09-628-495d-1  
Percent score: 32.54  
Sequence: 1 MDTLAVPTPGTIGSKLPV.....NHYHVVVVVHAEHLEMAV 613

Scoring table:  
Gapop 10.0, Gapext 0.5

Searched: 717574 gaps, 11197796 residues  
Total number of hits satisfying chosen parameters: 717574

Minimum DB seq length: 9  
Maximum DB seq length: 200000000

Post-processing: Minimum Match: 100%  
Listing first 45 summaries

Database:

Agroposeq\_042802:  
1: 1181 100.0 613 21 AAV02959 FAV  
2: 62101 100.0 613 22 AAV06645 FAV  
3: 62101 100.0 613 22 AAV06645 FAV  
4: 62101 100.0 613 22 AAV06645 FAV  
5: 62101 100.0 613 22 AAV06645 FAV  
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19: 62101 100.0 613 22 AAV06645 FAV  
20: 62101 100.0 613 22 AAV06645 FAV  
21: 62101 100.0 613 22 AAV06645 FAV  
22: 62101 100.0 613 22 AAV06645 FAV

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prioritized, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	Hit ID	Description
1	4255	100.0	613	21	AAV02959 FAV
2	4255	100.0	613	22	AAV06645 FAV
3	4255	100.0	613	22	AAV06645 FAV
4	3240	99.2	613	21	AAV02959 FAV
5	3240	99.2	613	21	AAV06645 FAV
6	3217	98.8	613	21	AAV06645 FAV
7	2894	88.9	554	22	AAH41784 FAV
8	2894	88.9	554	22	AAH47014 FAV
9	2894	88.9	554	22	AAH47014 FAV
10	2894	88.9	554	22	AAH47014 FAV
11	2894	88.9	554	22	AAH47014 FAV

12	2894	88.9	554	22	AAH47014 FAV
13	2894	88.9	554	22	AAH47014 FAV
14	2894	88.9	554	22	AAH47014 FAV
15	2894	88.9	554	22	AAH47014 FAV
16	2894	88.9	554	22	AAH47014 FAV
17	2894	88.9	554	22	AAH47014 FAV
18	2894	88.9	554	22	AAH47014 FAV
19	2894	88.9	554	22	AAH47014 FAV
20	2894	88.9	554	22	AAH47014 FAV
21	2894	88.9	554	22	AAH47014 FAV
22	2894	88.9	554	22	AAH47014 FAV
23	2894	88.9	554	22	AAH47014 FAV
24	2894	88.9	554	22	AAH47014 FAV
25	2894	88.9	554	22	AAH47014 FAV
26	2894	88.9	554	22	AAH47014 FAV
27	2894	88.9	554	22	AAH47014 FAV
28	2894	88.9	554	22	AAH47014 FAV
29	2894	88.9	554	22	AAH47014 FAV
30	2894	88.9	554	22	AAH47014 FAV
31	2894	88.9	554	22	AAH47014 FAV
32	2894	88.9	554	22	AAH47014 FAV
33	2894	88.9	554	22	AAH47014 FAV
34	2894	88.9	554	22	AAH47014 FAV
35	2894	88.9	554	22	AAH47014 FAV
36	2894	88.9	554	22	AAH47014 FAV
37	2894	88.9	554	22	AAH47014 FAV
38	2894	88.9	554	22	AAH47014 FAV
39	2894	88.9	554	22	AAH47014 FAV
40	2894	88.9	554	22	AAH47014 FAV
41	2894	88.9	554	22	AAH47014 FAV
42	2894	88.9	554	22	AAH47014 FAV
43	2894	88.9	554	22	AAH47014 FAV
44	2894	88.9	554	22	AAH47014 FAV
45	2894	88.9	554	22	AAH47014 FAV



















KM		CITY CA CANTON.	
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OS		Homo sapiens.	
XX			
IN		W02001 <sup>5</sup> /Z78 A2.	
XX			
FO	(9 AUG 2001:		
XX			
FE	+0 JAN 2001:	2001W0-0S00670.	
XX			
PK	(4 FEB 2000:	2000HS-01R0412-	
PR	-66 MAY 2000:	2000HS 0207456.	
FR	+0 JUN 2000:	2000HS 0608408.	
PK	(4 AUG 2000:	2000HS -0632464.	
PR	21 SEP 2000:	2000HS -0234687.	
FR	27 SEP 2000:	2000HS -0236459.	
PB	(4 OCT 2000:	2000CH-0024264.	
XX			
PA	(MOLEC.) MOLECULAR DYNAMICS INF		
XX			
X	POUN SEC.	HUMZEL DK.	CLAREN W.
XX			PAUL LBS;
FOR	REF.: 2001-100901/5A.		

The present invention relates to human single exon, particularly acid products (SHiNs; see A0110008 A0124455). The present sequence is a peptide encoded by the same protein. The SHiNs are derived from human fetal cells. The SHiNs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells, by measuring gene expression. The probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WHO at [http://who.int/junit/published/pet\\_sequences](http://who.int/junit/published/pet_sequences).

Seq	Sequenced	554	AA
Query Match		88.98%	Score 2804; EMBL 554
Fast Local Similarity		98.58%	Ident. No. 2205
Mutations	544	Conservative	3
		Mismatches	3
		Indels	4
		Gaps	1

[illegible][illegible][illegible]

	RESULT	13
AA0491	AA0491 standard; protein; 55d AA.	
XX		
XX	AA0491;	
XX		
XX	17-07-2001 (first entry)	
XX		
XX	negative #1523 checked by probe for measuring placental gene expression.	
XX		
KW	preterm microarray; human; placenta; antenatal diagnosis;	
KW	genetic disorder.	
XX		

XX	0000-8647(US)
XX	WZ2001-57-272-A-2.
FN	
XX	
FID	09-AT03-2001.
XX	
FF	30 JAN-2001; 2001bw-US00663.
XX	
FR	04 FEB-2000; 2000MS-0180312.
FR	26 MAY-2000; 2000MS-0200456.
FR	30-JUN-2000; 2000MS-0500408.
FR	03-AUG-2000; 2000MS-0632360.
FR	21 SEP-2000; 2000MS-0245087.
FR	27 SEP-2000; 2000MS-0246359.
FR	04-OCT-2000; 2000MS-0024263.
XX	
FA	(HEAD) RELEVANT DYNAMICS INC.
XX	
FI	Penn SG, Hanzel BK, Chen W, Rank BR;
XX	
XX	WEI: 2001-408897/53.
XX	

P1	Human genomic-derived single exon nucleotide acid probes, useful for
P1	analyzing gene expression in human placenta.
XX	
ES	Claim 27, SEQ ID No 30760, 654pp, English.
XX	
XX	The present invention relates to single exon nucleotide acid probes (GENE
02	see AAI34315-AA157540). The present sequence is a peptide encoded by one
02	such probe. The probes are useful for predicting a mutation for
02	predicting, mutation and displaying gene expression in samples derived
02	from human placenta. The probes are useful for neonatal diagnosis of
02	human genetic disorders.
XX	
XX	Sequence 554 AA.

[illegible]

[illegible][illegible]





















GeneCore version 4.5  
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00M protein - protein search, using SW model

Run on: September 4, 2002, 09:03:16, Search time 14.15 seconds  
(with last all hom. hits)  
1764.690 Million cell updates/sec

Title: US-09-628-495d-1  
Project score: 3256  
Sequence: 1 MDTTAVTPYGTCTCKLPD.....NTHVWVWEHHEHMAV 613

Scoring table: H4SDM62  
Gapop 10.0, Gapext 0.5

Searchop: 105224 seps, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1 SwissProt\_401\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	100.0	613	1	MILX_HUMAN
2	218	71.2	575	1	MILX_SHEEP
3	2234	68.6	583	1	MILX_MOUSE
4	937.5	28.8	345	1	MILX_CHICK
5	904.5	27.8	420	1	MILX_XENLA
6	891.5	27.4	350	1	MILX_HUMAN
7	887.5	27.3	353	1	MILX_MOUSE
8	886.5	27.2	353	1	MILX_CHICK
9	876.5	27.0	353	1	MILX_XENLA
10	854.5	26.7	466	1	MILX_SHEEP
11	854.5	26.2	462	1	MILX_HUMAN
12	797	24.5	289	1	MILX_CHICK
13	692	21.3	257	1	MILX_MOUSE
14	591	16.9	119	1	MILX_XENLA
15	465	14.3	151	1	MILX_HUMAN
16	434	13.3	156	1	MILX_MOUSE
17	424	13.0	154	1	MILX_CHICK
18	418	12.8	154	1	MILX_XENLA
19	416	12.9	152	1	MILX_HUMAN
20	411	12.6	157	1	MILX_MOUSE
21	409.5	12.4	152	1	MILX_CHICK
22	398	12.2	151	1	MILX_XENLA
23	350.5	10.4	432	1	MILX_HUMAN
24	345.5	10.3	432	1	MILX_MOUSE
25	341	10.5	429	1	MILX_CHICK
26	339	10.4	383	1	MILX_XENLA
27	338	10.4	522	1	MILX_HUMAN
28	336	10.3	508	1	MILX_MOUSE
29	332.5	10.2	420	1	MILX_CHICK
30	332.5	10.2	401	1	MILX_XENLA
31	332.5	10.2	401	1	MILX_HUMAN
32	331.5	10.2	401	1	MILX_MOUSE
33	331	10.2	398	1	MILX_CHICK

44	328	10.1	407	1	MILX_MOUSE
35	325	10.0	407	1	MILX_HUMAN
36	322.5	9.9	485	1	MILX_CHICK
37	321.5	9.9	485	1	MILX_XENLA
38	320.5	9.8	407	1	MILX_HUMAN
39	319.5	9.8	519	1	MILX_MOUSE
40	319	9.8	407	1	MILX_CHICK
41	317.5	9.8	485	1	MILX_XENLA
42	314	9.6	485	1	MILX_HUMAN
43	314	9.6	409	1	MILX_MOUSE
44	313.5	9.6	484	1	MILX_CHICK
45	311	9.6	446	1	MILX_XENLA

## ALIGNMENTS

RESULT 1					
MILX_HUMAN		STANDARD	INT	613 AA	
10	MILX_HUMAN				
AC	Q14985				
01	01 NOV 1997 (Ref. 35, latest update)				
02	01 NOV 1997 (Ref. 35, latest update)				
03	30 MAY 2000 (Ref. 39, latest update)				
04	Melatonin related receptor (19)				
05	gpr50				
06	Human sapiens (human)				
07	Human sapiens (human)				
08	Human sapiens (human)				
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00 Fukuyama: Metazoa: Chordata: Vertebrata: Euteleostomi:  
 01 Actinostriata: Aves: Neognathae: Galliformes: Phasianidae: Phasianinae:  
 02 Gallus:  
 03 MELT\_XENIA (c.f.).  
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Downloaded from <http://ajph.org/> on November 10, 2014

100

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-289 <NM2>  
A:Cross-references: EMBL:U06069, NID:q1050642; PDB:q1050963  
Kellin, P.; Yuan, H.; Sugimori, K.S.; Bahadur-Lazash, A.; Lee, F.J.S.; Pang, S.T.; Brown, E.B.; Jett, J.W. 239-278, 1995  
Title: Molecular and functional characterization of a partial cDNA encoding a novel G

RESULT 8  
162107  
melatonin receptor - rat (fragment)  
C) Specimen: Rat brain homogenate (Hofway Ltd)













27.38; Series 904.5; III 2; Length 420;

Fragment type	Interval
03-08-466-103A-12	

QUERCY MATCH, 27-48, SCORE 9:1-5; BB 2; Length 450;  
 Best Lateral Similarity 49.58; Prod. No. 9, 20-56;  
 MATCHES 161; Consistency .71; MATCHES 82; MATCHES 11; Gaps 3;

66. FVVSVSLVAMLVAVVYVYVIMHAKISGIMDLSQIQVQWVHTTGIISVGSVIFPNI VAVAIN 125

[illegible]

QY 186 EVTVTVVTHVVTELLVGVGVYVRVTRVYAARD ENGLDRINGLAEVENTRIMVIT 244  
 :  
DB 185 SAVVIIVVVVHTLVEMILVINVLKRIWHLVLVGSGRVRLGPKHLEPLDGFENVTMVEVF 244

[illegible]

TABLE 1. EFFECT OF VITAMIN E ON THE GROWTH OF *Y. enterocolitica* 429

Sequence 5, Applicant for US/08096165  
Patent No. 5949264  
GENERAL INFORMATION:  
AFFILIANT: boehringer, Max P.  
APPLICANT: Tardieu, Christopher

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ADDRESS: Zartley, McKee, Thornton, Woodruff & Sistrup  
STREET: 801 Grand Avenue, Suite 3200  
CITY: Los Molinos  
STATE: Iowa

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1  ZIP: 50309
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: MS DOS 3.30

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STEWART, EDWARD RELEASE #1-10, VOL 101 #1-10  
CURRENT APPLICATION DATA:  
ARRESTED: 5, 1993-94 #12, A, B, 46, 465  
FILING DATE: 18-JUL-1997  
CLASSIFICATION: 435

ADDRESS: H. ROBERT, 221 E. 72<sup>ND</sup> ST., 100  
 ELLING LANE, 19-JUL-1996  
 ADDRESS/DATE: H. ROBERT, 221 E. 72<sup>ND</sup> ST., 100  
 NAME: Robert, Heidi S.

REFERENCE: TEL: +86-0755-2593 1594  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 015-288-8667  
 TELEFAX: 515-286-1338  
 INFORMATION TO BE ATTACHED: 6





## INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 366 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-466-103A-4

Query Match: 26,79% Score 869.51 DB 2: Length 366  
 Best local similarity: 50.2% Pred. No. 3,56 54  
 Matches: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

DB 19 POLYPEPTIDE INFORMATION: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7  
 DB 37 PROTEIN: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

DB 79: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

DB 139: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

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DB 214: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

DB 255: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

DB 272: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

DB 315: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

DB 332: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

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DB 332: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 7

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## REFERENCE/US PAT. NUMBER: 15091

TELEPHONE: 615-288-4667  
 TELEFAX: 615-288-1334  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 366 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: cDNA  
 HYDROPHILIC: No  
 AND: CEREAL: No  
 ORIGINAL SOURCE:  
 FRAGMENT: ovine amino acids  
 CELL TYPE: Moladocyte  
 US-08-896-465-7

Query Match: 26,79% Score 869.51 DB 2: Length 366  
 Best local similarity: 50.2% Pred. No. 3,56 54  
 Matches: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 3

DB 19 POLYPEPTIDE INFORMATION: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 3  
 DB 37 PROTEIN: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 3

DB 79: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 3

DB 139: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 3

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DB 332: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 3

DB 332: 153: Conserved: 72: Mismatches: 71: Indels: 9: Gaps: 3

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CLASSIFICATION: 445
PUB APPLICATION DATA:
  APPLICATION NUMBER: 08/419,887
  FILING DATE: 07-Oct-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/201,857
    FILING DATE: 17-JUN-1994
    ATTORNEY/AGENT INFORMATION:
      NAME: Fraser, James K.
      REGISTRATION NUMBER: 44,819
      REFERENCE TO PRIOR APPLICATION:
        APPLICATION NUMBER: 08/201,857
        FILING DATE: 17-JUN-1994
        TELEPHONE: 617/542-5070
        TELEFAX: 617/542-8966
        INFORMATION FOR SEQ ID NO: 16:
          SEQUENCE CHARACTERISTICS:
            LENGTH: 462 amino acids
            TYPE: amino acid
            TOPOLOGY: linear
            MOLECULE TYPE: protein
            FRAGMENT TYPE: internal
            ORIGIN: 466-1034 bp

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Query Match: 26.28% Score 854.57 DB: 2: Length: 462
Best Local Similarity: 49.78% Prod. No: 436-534
Matches: 151; Conservative: 76; Mismatches: 66; Indels: 11; Gaps: 4;

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UY 17 KIDGPTVTFVATIMVAVITVIALIRGAVTAVKRRKAKKQKQIVVSSVAM 75
DB 42 KIRIRIVWALVATSSAVITVAVVGNLVTSVRSKRKRRKRELVSLATL 87
UY 76 IVALVYPIPLVAMSLQGMHISQIQGMVPTGLSVASSTFNVALAINRCYIGHSIQ 135
DB 88 VVALVYPIPLVAFVWALGEHRKASAPVWQISVGSFNDAIAINRCYIGHSMA 147
UY 146 YHREYVKNRTYLVITIMTIVAVIPMYIGTIEYDRTYCTINYNVIVTIVCT 195
DB 148 YHREYVKNRTYLVITIMTIVAVIPMYIGTIEYDRTYCTINYNVIVTIVCT 207
UY 196 HVALPILVGEYVIRVITVIAARDAIAPNPNOL---AEVRNLEVFTHLPAVWG 251
DB 208 HELLPAVVSFVTKRWIVILARKKA--KRSKQILASDLSRLIMFVVFATWMA 265
UY 252 FVAVLVAVVAKRKAKIEMVTLAAVTAIVNSCTAAVYVGLNSGKREVTWTFPA 311
DB 256 FVAVLVAVVAKRKAKIEMVTLAAVTAIVNSCTAAVYVGLNSGKREVTWTFPA 325
UY 312 MRRP 415
DB 426 LMSD 429

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RESULT: 11
US-08-466-1034-6
Sequence 6, Application US/084661034
Patent No. 5846124
GENERAL INFORMATION:
  APPLICANT: Koppert, Steven M.
  APPLICANT: Edisawa, Takashi
  TITLE OF INVENTION: HIGH ACTIVITY BETA-AIN
  TITLE OF INVENTION: RECEPTORS AND USES THEREOF
  NUMBER OF SEQUENCES: 29
  ADDRESSING ADDRESS:
    ADDRESS: 1180 & Richardson Hwy.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: US
    ZIP: 02110-2804
  OTHER READABLE FORM:
    METHOD TYPE: Diskette
    COUNTRY: IBM compatible

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OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
SUBJECT ATTENTION DATA:
  APPLICATION NUMBER: 08/287466, 1034
  FILING DATE: 06-JUN-1995
  CLASSIFICATION: 445
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/739,387
    FILING DATE: 07-Oct-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/251,857
    FILING DATE: 17-JUN-1994
    ATTORNEY/AGENT INFORMATION:
      NAME: Fraser, James K.
      REGISTRATION NUMBER: 44,819
      REFERENCE TO PRIOR APPLICATION:
        APPLICATION NUMBER: 08/251,857
        FILING DATE: 17-JUN-1994
        TELEPHONE: 617/542-5070
        TELEFAX: 617/542-8966
        INFORMATION FOR SEQ ID NO: 6:
          SEQUENCE CHARACTERISTICS:
            LENGTH: 288 amino acids
            TYPE: amino acid
            TOPOLOGY: linear
            MOLECULE TYPE: protein
            FRAGMENT TYPE: internal
            ORIGIN: 466-1034 bp

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Query Match: 22.78% Score 740.57 DB: 2: Length: 288
Best Local Similarity: 49.78% Prod. No: 440-457
Matches: 142; Conservative: 61; Mismatches: 72; Indels: 3; Gaps: 2;

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UY 63 GNFEVSIWAGMVAIVYPIPLVAMSLQGMHISQIQGMVPTGLSVASSTFNVAL 122
DB 1 GRTVYSAVADLVAVITVITLWKSIRKRRKRYVYVSGTLMOLVSGSTIRITGI 60
UY 123 AINRYVIGHSIQYERFVKNRTYLVITIMTIVAVIPMYIGTIEYDRTYCTINYN 182
DB 61 AINRYVIGHSIQYERFVKNRTYLVITIMTIVAVIPMYIGTIEYDRTYCTINYN 119
UY 192 LSNVITVITVGVHVALVAVVYVYVTKVLAAG--FAGDRDNGLAIVRTIRF 240
DB 120 VSSAVTAVVVFHVLVAVITVITLWKSIRKRRKRYVYVSGTLMOLVSGSTIRITGI 179
UY 241 VTLPAVWCPVAVVAVSFVKNRTYLVITIMTIVAVIPMYIGTIEYDRTYCTINYN 300
DB 180 VVYVFAVWALNTGLAVASGFAVYVRIHIVLVAVYVAVYVAVYVAVYVAVYV 249
UY 301 FRRVWTFVAMRHPITVIGLISIRE 328
DB 210 FRRVWTFVAVTAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 267

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RESULT: 11
US-08-866-465-8
Sequence 8, Application US/08896465
Patent No. 5949264
GENERAL INFORMATION:
  APPLICANT: Rothschild, Max F.
  APPLICANT: Ogley, Christopher A.
  APPLICANT: Mossor, Lori A.
  APPLICANT: Tuo-Ping, Yu
  TITLE OF INVENTION: GINS AND GININ MARKERS FOR IMPROVED
  TITLE OF INVENTION: REPRODUCTION IN ANIMALS
  NUMBER OF SEQUENCES: 25
  ADDRESSING ADDRESS:
    ADDRESS: 747 Ley, McKee, Theano, Weathers & Sasso
    STREET: 601 Grand Avenue, Suite 4200
    CITY: Des Moines
    STATE: Iowa
    COUNTRY: USA
    ZIP: 50309

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,365
FILING DATE: 18-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 69/322,180
FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S. 37,719
REGISTRATION NUMBER: 37,719
REFERENCE TO OTHER PAPER: 1996-031941
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
CELL TYPE: Melanocytic
US-08-896-365-H

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Query Match 2134, Score 692, DB 2, Length 257,
Best Local Similarity 49.28, Freq. No. 7,96-42,
Matches 119; Conservative 56; Mismatches 62; Indels 6; Gaps 2;

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QY 82 VYLMHMSIGWLSGCGQWGLIGLSVVSGLFVAVATNRYVYTHSYGTEPS 141
DB 1 YHAIASIVNWSSTFPAQSPHMSVLSVFNFTALINPVSCHPYRYS 60
QY 142 VNTTIVITMKTIVLAVLNMTGTEYERKTEFININPVTIVITV 201
DB 61 STNSICVYFLLIMLIVAVNLICVGTIOYPRYSCTFUSVSSATIAVVRHETVM 120
QY 202 LIAVTVYSIKVLAARDPACQNP - QIAVNRITTHVITLLVWTFYHVI 257
DB 121 LVVTVYFVAVLVVWVWV--FLESEFELEFEGEFHVAIVVIVVLAFLHFI 178
QY 258 VIVAVSPGPKKIPRMKYLAVYTAVERSCINAVYGLAERIKREKVTTHAKRPT 417
DB 179 LVAVASPMARITIMLVASTTRVTSGLALITGLNGRNGKERTFVAGV 208
QY 318 EF 419
DB 249 EF 210

```

```

RESULT 12
US-08-896-365-H
Sequence 9, Application US/08896365
Patent No. 6939264
GENERAL INFORMATION:
APPLICANT: ELLIOTT, Max E.
APPLICANT: Logano, Christopher K.
APPLICANT: Messer, Lori A.
APPLICANT: Tun-Ping, Yu
TITLE OF INVENTION: GENES AND THEIR POLYPEPTIDES IN A V.
TITLE OF INVENTION: RECOMBINANT TISSUE IN ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: 701 17th, MEYER, L.H.M.O. VANDERBILT 6, 37237

```

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STREET: 801 Grand Avenue, Suite 4200
CITY: Des Moines
STATE: Iowa
COUNTRY: USA
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,365
FILING DATE: 18-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 69/322,180
FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S. 37,719
REGISTRATION NUMBER: 37,719
REFERENCE TO OTHER PAPER: 1996-031941
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
CELL TYPE: Melanocytic
US-08-896-365-H

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Query Match 1218, Score 394, DB 2, Length 153,
Best Local Similarity 45.29, Freq. No. 4,86-21,
Matches 70; Conservative 39; Mismatches 40; Indels 6; Gaps 3;

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QY 127 VYVTHSLDYPRISVARE--GVYVITWIMVAVLNWYETEDPDTYTCINYN 184
DB 1 VYVTHSLDYPRISVARE--GVYVITWIMVAVLNWYETEDPDTYTCINYN 184
QY 185 RIVVITVTHVYVILVWYVYKIVWYKIVLAARCA GQRDQGLAVRNLTFEV 242
DB 59 SSAYTIAVVEFVAVPVVFRVIRVAVVLDLRKAKPPNNRKLQDPFRNVTMFV 118
QY 243 ELIAVWTFINVLIVAVSRKQACKIPRWYLT 277
DB 119 LVIAVFWAFLNIGLAVASPMARITPMLPV 153

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RESULT 13
US-09-255-668-H
Sequence 2, Application US/09255668
Patent No. 6262246
GENERAL INFORMATION:
APPLICANT: Gerald, Christopher P.G.
APPLICANT: Jones, Kenneth A.
APPLICANT: Bouillon, James A.
APPLICANT: Bouillon, Beth
TITLE OF INVENTION: 626 Encoding Mammalian Neutrophils IF (NPEF) Receptors
FILE REFERENCE: 1795/57155-A
PUBLICATION NO. IN PUBL. NO. 255,368
CURRENT FILING DATE: 1999-02-22
PUBLICATION DATE: 2000-10-11
PUBLISHER FILING DATE: 1998-09-25
NUMBER OF SEQ. ID NOs: 12

```





00 274 EKMLLIVALLTISMPLETTMMSTADLSNNH 01NNYTTFAHGLAONNNVP 340  
07 292 VLYULMREHREBYWTTHARSHLITTFOLLOHKEHODANTHAKAHAKOANEDOR 351  
00 341 LYGFENENFERGF-----GEAFOLLOLOKARPM ---E 461  
07 352 AUAOTAVHHTHNNVNTLPNMAAHEDHAKNNKHRESEAVYKSA 400  
00 362 AVA YFZHWYINZSLV -HNT-2H03 ETUJHFA 499

Search completed: September 4, 2002, 09:02:41  
Job time: 255 Sec

